

In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 7, line 21 to page 8, line 3 and replace it with the following paragraph:

Figure 3 shows bisulfite sequencing analysis of VT and TT somatic tissues in Example 1. (A) Schematic representation of the *hMLH1* locus showing the locations of the A, B, and C regions in relation to the region sequenced (dotted lines). (B) Sequence of *hMLH1* (**SEQ ID NO: 17**) within the dotted region defined in (A). The primers used to amplify this region are underlined. CpG doublets within this domain are highlighted in bold and numbered 1 through 17. The single nucleotide polymorphism is also highlighted with G and A shown in larger text. (C) This figure shows the results of bisulfite allelic sequencing in the various somatic tissues of TT and VT. Black and white squares represent individual CpGs and are numbered according to their location in the sequence shown in (B). Grey or white circles represent the A or G genotype, respectively. Each horizontal row of squares represents the results from individual alleles. In both patient TT and VT, the hypermethylated alleles are always of the G genotype, whereas the A alleles show patchy methylation only and are never hypermethylated. Mosaicism was evident in the hair follicles of TT, and in all tissues from VT, as evidenced by the hypomethylation of the occasional G allele.